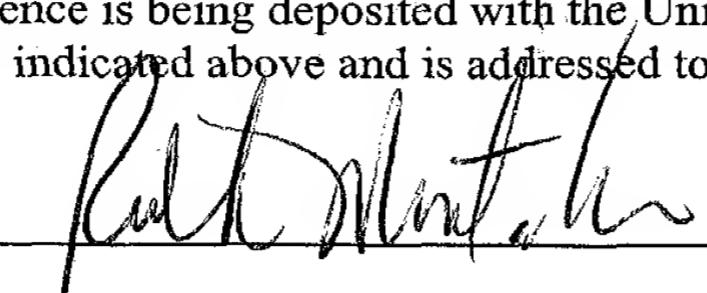


#12 | Reconsiderati
8/8/02

EXPRESS MAIL No.: EV 168 019 864 US

Deposited: July 23, 2002

I hereby certify that this correspondence is being deposited with the United States Postal Service Express mail under 37 CFR 1.10 on the date indicated above and is addressed to: Assistant Commissioner for Patents, Washington, DC 20231



/ Ruth Montalvo

Date: 07/23/02

In the event that this paper is late filed and a necessary Petition for an Extension of Time is not concurrently filed herewith, please consider this as a Petition for the requisite extension of time, and to the extent not tendered by check attached hereto, authorization to charge the extension fee, or any other fee required in connection with this paper, to Deposit Account No. 50-1529.



Docket No. GK-GEY-1083C/500350.20082

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

RECEIVED

AUG 05 2002

Applicants: Thomas Cremer et al

Group:

Serial No.: 09/773,647

TECH CENTER 1600/29

Filed: January 31, 2001

Examiner: J. Fredman

For: ARRANGEMENT OF NUCLEIC ACID SEQUENCES AND IT'S USE

Commissioner of Patents
Washington, D. C. 20231

RESPONSE

SIR:

This is in response to the Office Action mailed February 1, 2002.

Reconsideration and withdrawal of the rejection of claims 1-5 and 7 as being anticipated under 35 USC 102 (e) by the Chrapko et al '270 patent are respectfully requested. The Examiner asserts that Chrapko '270 teaches an element comprising a supporting matrix such as a glass slide which has target nucleic acid sequences attached using a thin polyacrylamide film and that these are placed in a geometric arrangement in parallel rows. The Examiner further asserts that the nucleic acids of Chrapko are structurally identical to the short cDNA probes and inherently comprise such probes. However, it is submitted that the Examiner's characterization of Chrapko et al is incorrect. In particular, the present invention as claimed constitutes an analytical element which can be used to analyze genomic variations by comparative genomic hybridization and is composed of a target nucleic acid sequences which are fixed onto a supporting matrix in a specific geometric arrangement. Thus, in contrast to the disclosure of Chrapko et al '270 and as shown in Fig. 1 of that reference, the "geometric arrangement" of the target nucleic acid sequence of the present invention is not

merely the geometric arrangement of specific identical units or targets of the nucleic acid. Rather, the geometric arrangement relates to different target nucleic acids which are presented in a specific geometric arrangement. In other words, it is the target nucleic acid sequences which are different and together they are fixed in a specific geometric arrangement one to the other. In contrast, Chrapko et al indicates that the only geometricity to the arrangement is the physical arrangement of the individual deposits of the acrylamide. Each such deposit however contains essentially the same oligonucleotides. This is a basic difference from the present invention as claimed where it is the arrangement of the different target nucleic acid which is specified.

Thus, Chrapko et al does not teach such a specific geometric arrangement of the particular target nucleic acid sequences one relative the other. Rather, Chrapko et al makes no distinction what so ever as to any given "array" of target nucleic acid sequences. Thus, the arrays are positioned geometrically on the slide but each array is essentially the same. The reference neither discloses nor in any way suggests the placement of different types of arrays in different geometric positions on the slide. And this rejection should be withdrawn.

Similarly, reconsideration and withdrawal of the rejection of claims 1-3, 6 and 8-14 as being anticipated under 35 USC 102 (b) by the Bernheim et al article are also requested. The Examiner asserts that Bernheim teaches an element which comprises the supporting matrix of nitrocellulose (referring to Figure 5) each of which have the 24 human chromosomes sorted into peaks, 1 Y peak and 1 non-Y peak, attached to the nitrocellulose support. The Examiner further asserts that it shows that these are placed in a geometric arrangement and the Examiner additionally asserts that the chromosomes attached to the nitrocellulose since they are whole chromosomes are inherently arranged in P to Q order. The Examiner further notes that the two peaks attached to the nitrocellulose comprise every single human chromosome including 13, 18, 21, X and Y inherently and that the two peaks which are attached to the nitrocellulose also inherently comprise chromosome bands. Hereagain, however, it is believed that this characterization of the Bernheim article is not correct insofar as it's disclosing the presently claimed invention.

However, the disclosure in Bernheim with respect to the placement of the 24 human chromosomes sorted into peaks refers solely to the whole chromosome individually located at a specific point on the nitrocellulose. There is absolutely no indication in the reference that the target nucleic acid sequences are arranged from top to bottom corresponding to their physical

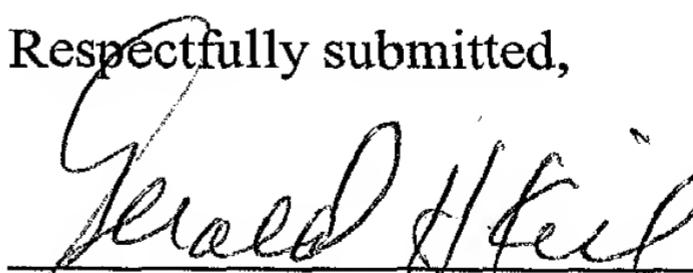
arrangement on a chromosome from P to Q. Thus, a fundamental difference between the Bernheim paper and that of the present invention is that with Bernheim, each filter carries a single dot containing the DNA of a single peak. While each dot may contain DNA of different chromosomes, the DNA are not arranged in a spatially separated manner but are intermingled with the single dot. Certainly, Fig. 5 does not show anything else but only the compared set of different filters loaded with different amounts of DNA in each peak wherein each filter contains only a single dot.

In particular, the article generally refers to the sorting of human chromosomes for identifying and isolating the Y-chromosome in order to discriminate between male and female cells. The isolation and sorting of the different chromosomes is performed according to the different peaks identified in the fluorometrical analysis. The single peaks do not necessarily correspond to single chromosomes since the resolution is apparently a limiting factor. The DNA of the two identified peaks is then transferred to nitrocellulose and hybridized with probes specific for male/female DNA for analysis.

Consequently, the reference simply does not disclose a specific geometrical arrangement of different DNA species on a single filter as required by the present claims. The reference therefore neither discloses nor remotely suggests the present invention as claimed and this rejection should also be withdrawn.

In view of the foregoing, it is submitted that this application is in condition for allowance and favorable reconsideration and prompt notice of allowance are earnestly solicited.

Respectfully submitted,



Gerald H. Kiel – Reg. No. 25,116 for
Jules E. Goldberg - Reg. No. 24,408
Reed Smith LLP
599 Lexington Avenue, 29th Floor
New York, NY 10022
Tel. (212) 521-5403

JEG:dej